



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 12:26 PM BST

PDB ID : 5ZQK
Title : Dengue Virus Non Structural Protein 5
Authors : El Sahili, A.; Soh, T.S.; Schiltz, J.; Gharbi-Ayachi, A.; Goh, B.C.; Seh, C.C.;
Dedon, P.C.; Shi, P.Y.; Lim, S.P.; Lescar, J.
Deposited on : 2018-04-19
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

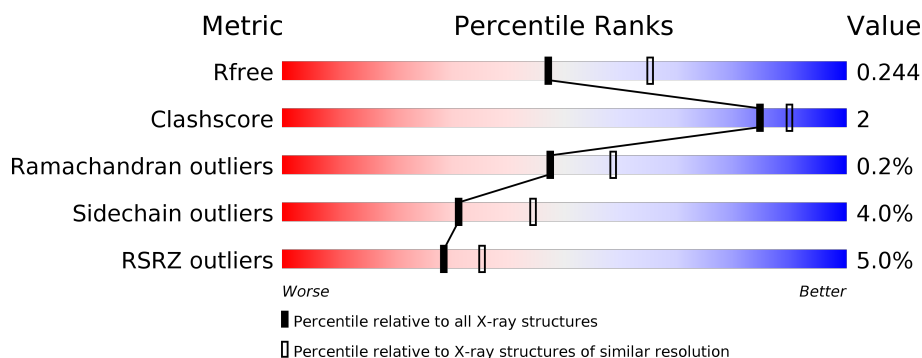
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	923	<div> <div>6%</div> <div> <div></div> <div>87%</div> <div>7%</div> <div>5%</div> </div> </div>
1	B	923	<div> <div>4%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>5%</div> </div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15082 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Non Structural Protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	874	Total	C	N	O	S	0	1	0
			7044	4428	1264	1307	45			
1	B	875	Total	C	N	O	S	0	3	0
			7065	4442	1268	1310	45			

There are 46 discrepancies between the modelled and reference sequences:

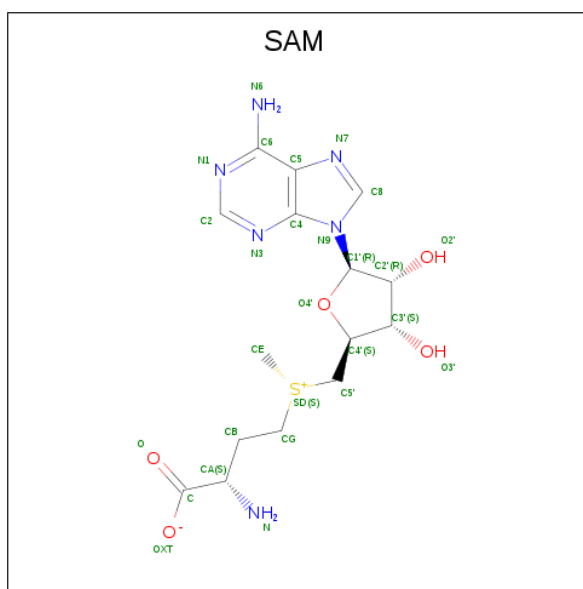
Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	expression tag	UNP H9M652
A	-21	HIS	-	expression tag	UNP H9M652
A	-20	HIS	-	expression tag	UNP H9M652
A	-19	HIS	-	expression tag	UNP H9M652
A	-18	HIS	-	expression tag	UNP H9M652
A	-17	HIS	-	expression tag	UNP H9M652
A	-16	HIS	-	expression tag	UNP H9M652
A	-15	SER	-	expression tag	UNP H9M652
A	-14	SER	-	expression tag	UNP H9M652
A	-13	GLY	-	expression tag	UNP H9M652
A	-12	VAL	-	expression tag	UNP H9M652
A	-11	ASP	-	expression tag	UNP H9M652
A	-10	LEU	-	expression tag	UNP H9M652
A	-9	GLY	-	expression tag	UNP H9M652
A	-8	THR	-	expression tag	UNP H9M652
A	-7	GLU	-	expression tag	UNP H9M652
A	-6	ASN	-	expression tag	UNP H9M652
A	-5	LEU	-	expression tag	UNP H9M652
A	-4	TYR	-	expression tag	UNP H9M652
A	-3	PHE	-	expression tag	UNP H9M652
A	-2	GLN	-	expression tag	UNP H9M652
A	-1	SER	-	expression tag	UNP H9M652
A	0	MET	-	expression tag	UNP H9M652
B	-22	MET	-	expression tag	UNP H9M652
B	-21	HIS	-	expression tag	UNP H9M652

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	HIS	-	expression tag	UNP H9M652
B	-19	HIS	-	expression tag	UNP H9M652
B	-18	HIS	-	expression tag	UNP H9M652
B	-17	HIS	-	expression tag	UNP H9M652
B	-16	HIS	-	expression tag	UNP H9M652
B	-15	SER	-	expression tag	UNP H9M652
B	-14	SER	-	expression tag	UNP H9M652
B	-13	GLY	-	expression tag	UNP H9M652
B	-12	VAL	-	expression tag	UNP H9M652
B	-11	ASP	-	expression tag	UNP H9M652
B	-10	LEU	-	expression tag	UNP H9M652
B	-9	GLY	-	expression tag	UNP H9M652
B	-8	THR	-	expression tag	UNP H9M652
B	-7	GLU	-	expression tag	UNP H9M652
B	-6	ASN	-	expression tag	UNP H9M652
B	-5	LEU	-	expression tag	UNP H9M652
B	-4	TYR	-	expression tag	UNP H9M652
B	-3	PHE	-	expression tag	UNP H9M652
B	-2	GLN	-	expression tag	UNP H9M652
B	-1	SER	-	expression tag	UNP H9M652
B	0	MET	-	expression tag	UNP H9M652

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Zn	0	0
			2	2		
4	A	2	Total	Zn	0	0
			2	2		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total	Mg	0	0
			2	2		

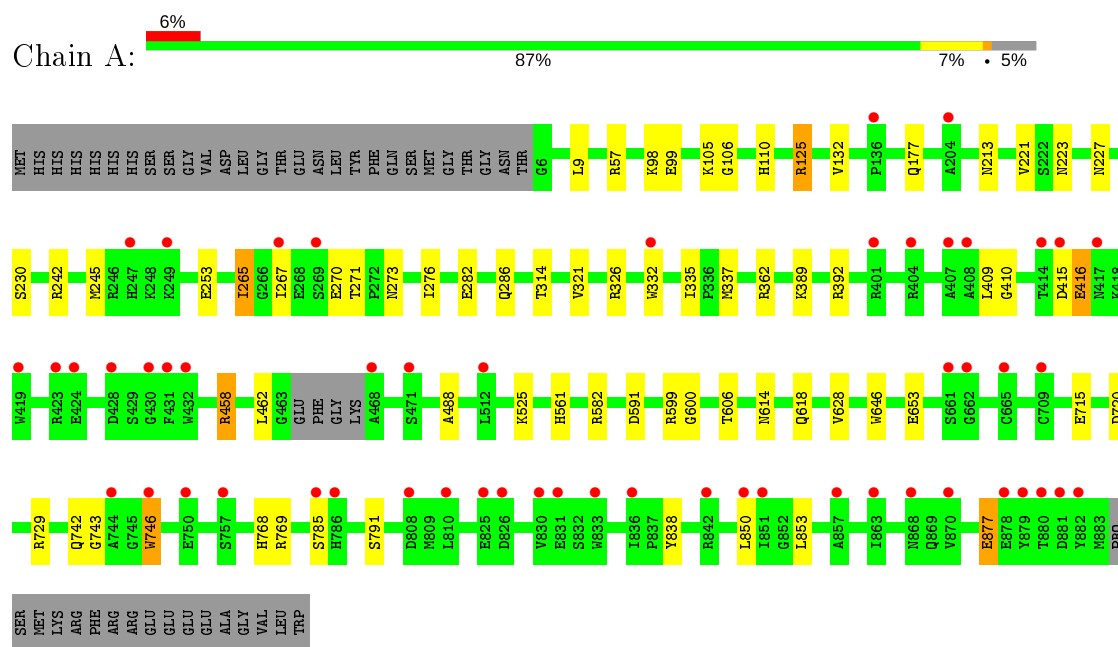
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	457	Total	O	0	0
			457	457		
7	B	436	Total	O	0	0
			436	436		

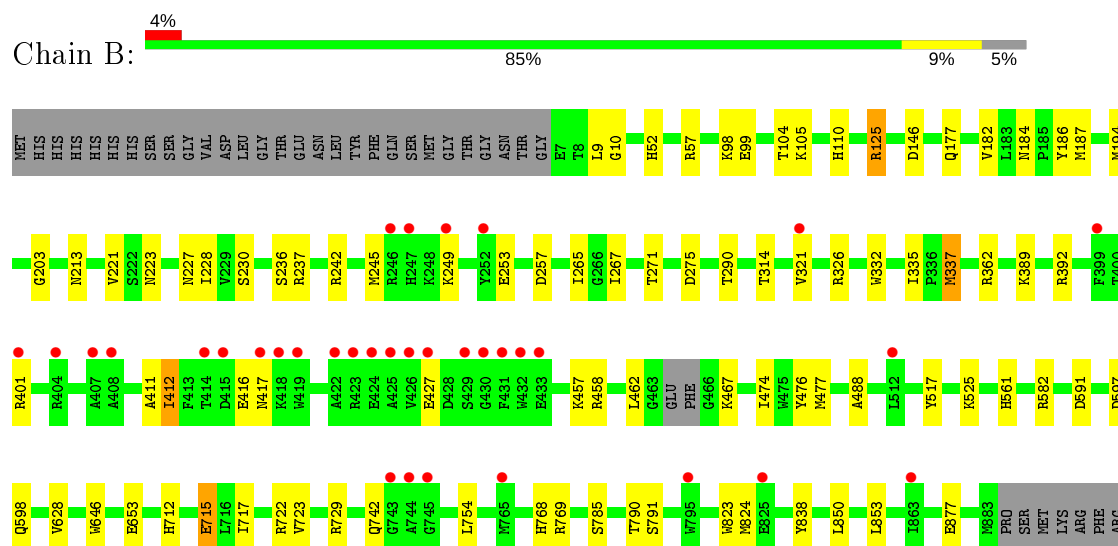
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Non Structural Protein 5



• Molecule 1: Non Structural Protein 5



ARG
GLU
GLU
GLU
GLU
ALA
GLY
VAL
LEU
TRP

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.68 Å 146.10 Å 97.24 Å 90.00° 105.45° 90.00°	Depositor
Resolution (Å)	46.00 – 2.30 44.62 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.00-2.30) 99.7 (44.62-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.29 Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.196 , 0.235 0.202 , 0.244	Depositor DCC
R_{free} test set	5152 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.7	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15082	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, MG, SAM, EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.51	0/7204	0.71	0/9731
1	B	0.51	0/7228	0.71	0/9761
All	All	0.51	0/14432	0.71	0/19492

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7044	0	6943	26	0
1	B	7065	0	6973	38	0
2	A	27	0	22	1	0
2	B	27	0	22	2	0
3	A	6	0	8	1	0
3	B	6	0	8	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	4	0	6	0	0
5	B	4	0	6	3	0
6	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	457	0	0	2	0
7	B	436	0	0	3	0
All	All	15082	0	13988	64	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (64) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:227:ASN:HD22	1:B:230:SER:H	1.35	0.72
1:A:227:ASN:HD22	1:A:230:SER:H	1.37	0.72
1:B:290:THR:HG22	7:B:1304:HOH:O	1.89	0.72
1:A:213:ASN:HD21	1:A:242:ARG:HH11	1.38	0.71
1:B:213:ASN:HD21	1:B:242:ARG:HH11	1.36	0.71
1:B:237:ARG:HH12	5:B:1007:EDO:H12	1.56	0.70
1:A:177:GLN:HE22	1:A:223:ASN:HD21	1.42	0.67
1:A:582:ARG:HD3	1:A:591:ASP:OD2	1.94	0.67
1:B:582:ARG:HD3	1:B:591:ASP:OD2	1.94	0.67
1:A:282:GLU:O	1:A:286:GLN:HG2	1.97	0.65
1:A:99:GLU:HG3	1:A:125:ARG:HH21	1.64	0.63
1:B:177:GLN:HE22	1:B:223:ASN:HD21	1.44	0.62
1:B:754:LEU:HD13	1:B:791:SER:HB3	1.83	0.60
1:B:457:LYS:HB2	1:B:474:ILE:HG12	1.84	0.60
1:B:99:GLU:HG3	1:B:125:ARG:HH21	1.67	0.59
1:A:106:GLY:O	1:A:110:HIS:HB2	2.03	0.58
1:B:182:VAL:HG21	1:B:194:MET:HE3	1.86	0.57
1:A:321:VAL:HG11	1:A:326:ARG:HD2	1.86	0.57
1:A:332:TRP:HA	1:A:335:ILE:HD12	1.87	0.57
1:B:332:TRP:HA	1:B:335:ILE:HD12	1.87	0.56
1:A:769:ARG:HH11	1:A:769:ARG:HG2	1.70	0.55
1:B:769:ARG:HH11	1:B:769:ARG:HG2	1.70	0.55
1:A:273:ASN:HD22	1:A:276:ILE:HG12	1.72	0.55
1:B:321:VAL:HG11	1:B:326:ARG:HD2	1.88	0.54
1:A:458:ARG:HH21	1:A:743:GLY:HA2	1.73	0.54
1:A:242:ARG:HA	1:A:245:MET:HG2	1.89	0.54
1:B:597:ASP:O	1:B:598:GLN:HB2	2.07	0.53
1:A:746:TRP:HA	1:A:746:TRP:CE3	2.44	0.53
1:B:337:MET:HB3	7:B:1494:HOH:O	2.08	0.52
1:B:768:HIS:HA	1:B:838:TYR:HA	1.93	0.51
1:A:488:ALA:O	1:A:561:HIS:HE1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:768:HIS:HA	1:A:838:TYR:HA	1.94	0.50
1:B:146:ASP:HB3	2:B:1001:SAM:HG1	1.94	0.49
1:B:9:LEU:HB3	1:B:236:SER:HB3	1.92	0.49
1:B:52:HIS:HD2	1:B:257:ASP:OD1	1.95	0.48
1:B:488:ALA:O	1:B:561:HIS:HE1	1.96	0.48
1:A:410:GLY:HA3	7:A:1196:HOH:O	2.15	0.46
1:B:412:ILE:HA	1:B:477:MET:O	2.16	0.45
1:B:411:ALA:HB1	1:B:476:TYR:CD2	2.53	0.44
1:A:614:ASN:O	1:A:618:GLN:HG2	2.17	0.44
1:B:628:VAL:HG21	1:B:646:TRP:CD1	2.53	0.44
1:A:877:GLU:HA	7:A:1391:HOH:O	2.17	0.42
1:B:411:ALA:HB1	1:B:476:TYR:CG	2.54	0.42
1:A:132:VAL:HG13	2:A:1001:SAM:H2	2.01	0.42
1:B:98:LYS:HA	1:B:265:ILE:HG12	2.01	0.42
1:A:600:GLY:HA2	3:A:1002:GOL:O3	2.19	0.42
1:A:599:ARG:HG2	1:A:606:THR:HG23	2.00	0.42
1:B:850:LEU:O	1:B:853:LEU:HB2	2.20	0.42
1:A:227:ASN:ND2	1:A:230:SER:H	2.12	0.42
1:B:203:GLY:HA3	1:B:221:VAL:O	2.20	0.41
1:B:517:TYR:HB3	1:B:823:TRP:CE2	2.54	0.41
1:B:712:HIS:HD2	7:B:1493:HOH:O	2.03	0.41
1:A:628:VAL:HG21	1:A:646:TRP:CD1	2.54	0.41
1:B:457:LYS:HD2	1:B:474:ILE:HD11	2.03	0.41
1:B:184:ASN:OD1	1:B:187:MET:HG2	2.20	0.41
1:B:237:ARG:HH22	5:B:1007:EDO:H12	1.86	0.41
1:B:715:GLU:HG2	1:B:723:VAL:CG1	2.50	0.41
1:A:98:LYS:HA	1:A:265:ILE:HG12	2.03	0.41
1:B:227:ASN:ND2	1:B:230:SER:H	2.10	0.41
1:A:850:LEU:O	1:A:853:LEU:HB2	2.21	0.41
1:B:237:ARG:NH1	5:B:1007:EDO:H12	2.32	0.41
1:B:10:GLY:HA3	1:B:186:TYR:CG	2.56	0.40
1:B:722:ARG:HD2	1:B:824:MET:SD	2.61	0.40
1:B:110:HIS:HD2	2:B:1001:SAM:O2'	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	871/923 (94%)	840 (96%)	29 (3%)	2 (0%)	47	58
1	B	874/923 (95%)	843 (96%)	30 (3%)	1 (0%)	51	64
All	All	1745/1846 (94%)	1683 (96%)	59 (3%)	3 (0%)	47	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	416	GLU
1	B	467	LYS
1	A	791	SER

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	759/800 (95%)	730 (96%)	29 (4%)	33	47
1	B	762/800 (95%)	730 (96%)	32 (4%)	30	42
All	All	1521/1600 (95%)	1460 (96%)	61 (4%)	31	44

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	57	ARG
1	A	105	LYS

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Mol	Chain	Res	Type
1	A	125	ARG
1	A	221	VAL
1	A	253	GLU
1	A	265	ILE
1	A	267	ILE
1	A	270	GLU
1	A	271	THR
1	A	314	THR
1	A	337	MET
1	A	362	ARG
1	A	389	LYS
1	A	392	ARG
1	A	409	LEU
1	A	415	ASP
1	A	416	GLU
1	A	458	ARG
1	A	462	LEU
1	A	525	LYS
1	A	653	GLU
1	A	715	GLU
1	A	720	ASP
1	A	729	ARG
1	A	742	GLN
1	A	746	TRP
1	A	785	SER
1	A	877	GLU
1	B	57	ARG
1	B	104	THR
1	B	105	LYS
1	B	125	ARG
1	B	228	ILE
1	B	245	MET
1	B	249	LYS
1	B	253	GLU
1	B	267	ILE
1	B	271	THR
1	B	275	ASP
1	B	314	THR
1	B	337	MET
1	B	362	ARG
1	B	389	LYS
1	B	392	ARG

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Mol	Chain	Res	Type
1	B	401	ARG
1	B	412	ILE
1	B	416	GLU
1	B	417	ASN
1	B	427	GLU
1	B	458	ARG
1	B	462	LEU
1	B	525	LYS
1	B	653	GLU
1	B	715	GLU
1	B	717	ILE
1	B	729	ARG
1	B	742	GLN
1	B	785	SER
1	B	790	THR
1	B	877	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	ASN
1	A	110	HIS
1	A	127	GLN
1	A	170	ASN
1	A	213	ASN
1	A	223	ASN
1	A	227	ASN
1	A	273	ASN
1	A	513	HIS
1	A	555	ASN
1	A	561	HIS
1	A	622	GLN
1	A	633	GLN
1	A	634	GLN
1	A	712	HIS
1	A	760	GLN
1	A	786	HIS
1	A	862	ASN
1	B	52	HIS
1	B	96	ASN
1	B	110	HIS
1	B	170	ASN

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Mol	Chain	Res	Type
1	B	213	ASN
1	B	223	ASN
1	B	227	ASN
1	B	288	HIS
1	B	351	GLN
1	B	555	ASN
1	B	561	HIS
1	B	622	GLN
1	B	633	GLN
1	B	634	GLN
1	B	712	HIS
1	B	760	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SAM	B	1001	-	21,29,29	0.68	0	18,42,42	0.93	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SAM	A	1001	-	21,29,29	0.65	0	18,42,42	0.92	1 (5%)
5	EDO	B	1007	-	3,3,3	0.76	0	2,2,2	0.29	0
3	GOL	B	1002	-	5,5,5	0.08	0	5,5,5	0.25	0
3	GOL	A	1002	-	5,5,5	0.11	0	5,5,5	0.25	0
5	EDO	A	1005	-	3,3,3	0.53	0	2,2,2	0.47	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SAM	B	1001	-	-	0/8/33/33	0/3/3/3
2	SAM	A	1001	-	-	0/8/33/33	0/3/3/3
5	EDO	B	1007	-	-	0/1/1/1	-
3	GOL	B	1002	-	-	1/4/4/4	-
3	GOL	A	1002	-	-	2/4/4/4	-
5	EDO	A	1005	-	-	0/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	SAM	C5-C6-N6	2.42	124.03	120.35
2	B	1001	SAM	C5-C6-N6	2.16	123.64	120.35

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1002	GOL	C1-C2-C3-O3
3	A	1002	GOL	O2-C2-C3-O3
3	B	1002	GOL	C1-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 7 short contacts:

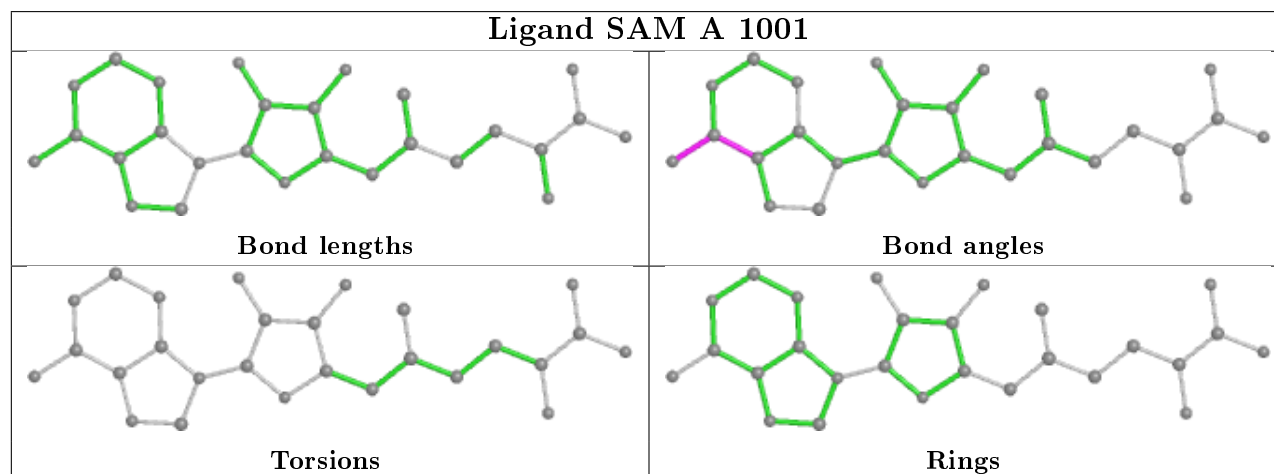
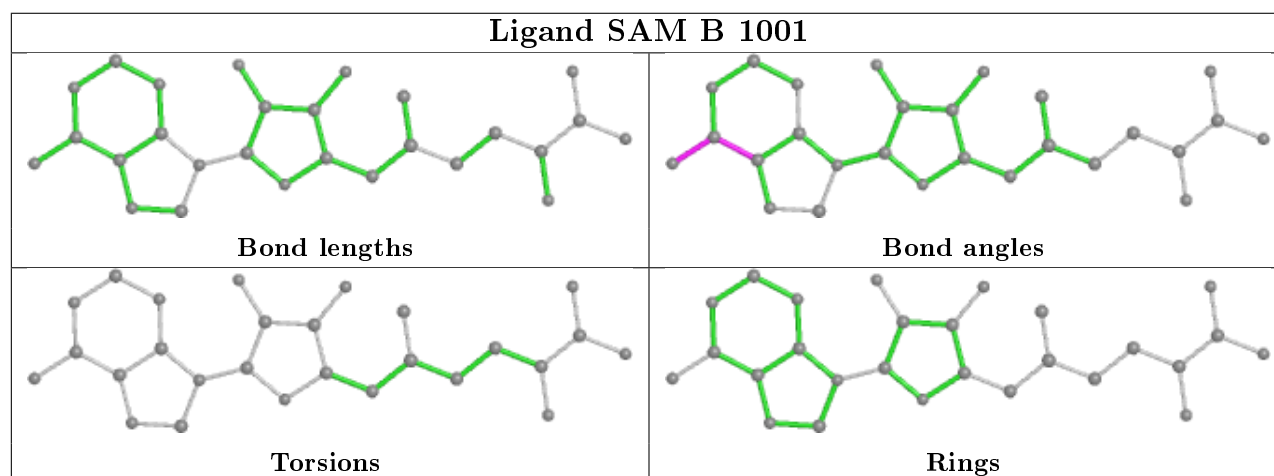
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	SAM	2	0
2	A	1001	SAM	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1007	EDO	3	0
3	A	1002	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	874/923 (94%)	0.48	54 (6%)	20 26	36, 56, 91, 125	0
1	B	875/923 (94%)	0.37	34 (3%)	39 46	39, 56, 89, 118	0
All	All	1749/1846 (94%)	0.43	88 (5%)	28 35	36, 56, 90, 125	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	744	ALA	9.8
1	A	882	TYR	8.4
1	A	744	ALA	6.9
1	B	247	HIS	6.9
1	A	880	THR	5.1
1	B	743	GLY	5.0
1	B	745	GLY	4.9
1	B	246	ARG	4.3
1	B	249	LYS	4.3
1	A	471	SER	4.2
1	A	414	THR	3.8
1	A	419	TRP	3.7
1	A	833	TRP	3.7
1	A	830	VAL	3.7
1	A	863	ILE	3.6
1	B	419	TRP	3.6
1	A	428	ASP	3.4
1	A	269	SER	3.4
1	A	879	TYR	3.4
1	B	423	ARG	3.3
1	A	786	HIS	3.3
1	B	414	THR	3.3
1	A	836	ILE	3.2
1	B	426	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	427	GLU	3.1
1	A	407	ALA	3.1
1	A	267	ILE	3.1
1	B	408	ALA	3.1
1	B	432	TRP	3.0
1	A	401	ARG	2.9
1	A	247	HIS	2.9
1	A	857	ALA	2.9
1	B	407	ALA	2.9
1	A	757	SER	2.9
1	B	431	PHE	2.8
1	A	430	GLY	2.8
1	B	415	ASP	2.8
1	B	765	MET	2.8
1	A	808	ASP	2.8
1	A	881	ASP	2.7
1	B	417	ASN	2.7
1	B	512	LEU	2.7
1	B	422	ALA	2.7
1	A	431	PHE	2.6
1	A	249	LYS	2.6
1	B	430	GLY	2.6
1	A	512	LEU	2.6
1	A	785	SER	2.5
1	A	810	LEU	2.5
1	B	401	ARG	2.5
1	A	746	TRP	2.5
1	B	424	GLU	2.5
1	A	662	GLY	2.5
1	A	870	VAL	2.4
1	A	709	CYS	2.4
1	A	831	GLU	2.4
1	A	878	GLU	2.4
1	B	418	LYS	2.4
1	A	415	ASP	2.4
1	A	432	TRP	2.4
1	A	661	SER	2.4
1	A	825	GLU	2.4
1	B	404	ARG	2.4
1	A	424	GLU	2.3
1	A	417	ASN	2.3
1	A	423	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	252	TYR	2.3
1	A	851	ILE	2.3
1	A	136	PRO	2.2
1	A	665	CYS	2.2
1	B	425	ALA	2.2
1	A	868	ASN	2.2
1	A	826	ASP	2.2
1	B	429	SER	2.2
1	B	433	GLU	2.1
1	A	408	ALA	2.1
1	A	468	ALA	2.1
1	A	842	ARG	2.1
1	B	825	GLU	2.1
1	A	332	TRP	2.1
1	B	399	PHE	2.1
1	A	404	ARG	2.0
1	A	850	LEU	2.0
1	A	750	GLU	2.0
1	B	795	TRP	2.0
1	B	321	VAL	2.0
1	B	863	ILE	2.0
1	A	204	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	MG	B	1003	1/1	0.76	0.28	80,80,80,80	0

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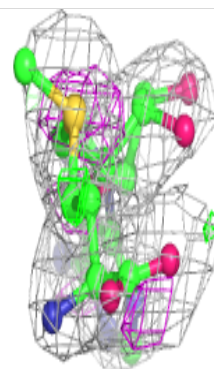
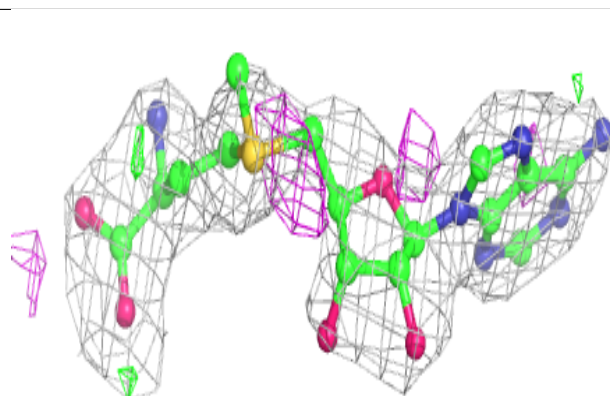
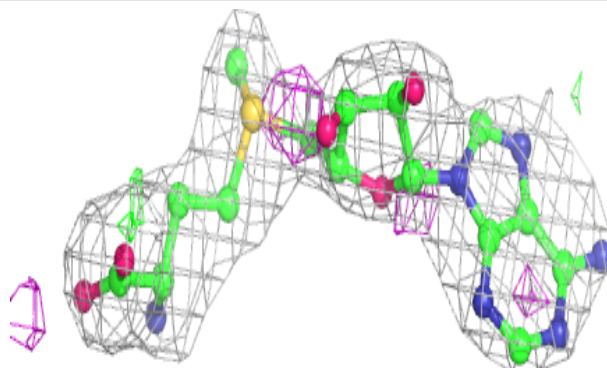
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SAM	B	1001	27/27	0.88	0.24	60,74,79,80	0
6	MG	B	1004	1/1	0.88	0.26	75,75,75,75	0
3	GOL	A	1002	6/6	0.90	0.28	63,65,65,66	0
5	EDO	B	1007	4/4	0.90	0.22	43,51,58,62	0
5	EDO	A	1005	4/4	0.92	0.54	72,73,74,74	0
3	GOL	B	1002	6/6	0.94	0.18	52,57,58,61	0
2	SAM	A	1001	27/27	0.94	0.17	49,57,63,66	0
4	ZN	B	1005	1/1	0.99	0.13	52,52,52,52	0
4	ZN	B	1006	1/1	0.99	0.15	57,57,57,57	0
4	ZN	A	1003	1/1	1.00	0.16	55,55,55,55	0
4	ZN	A	1004	1/1	1.00	0.14	53,53,53,53	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

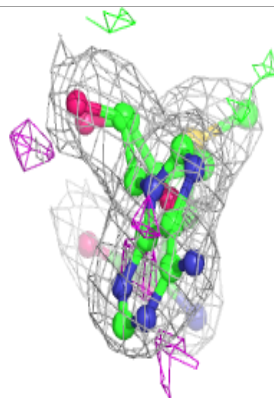
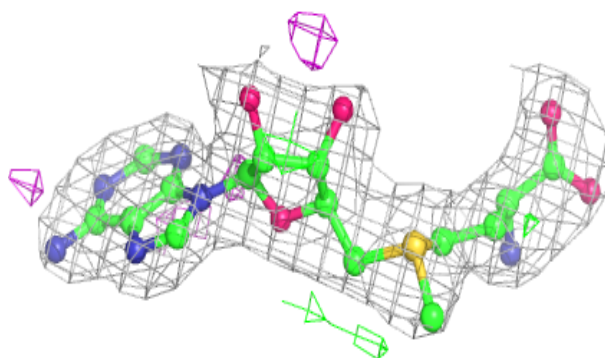
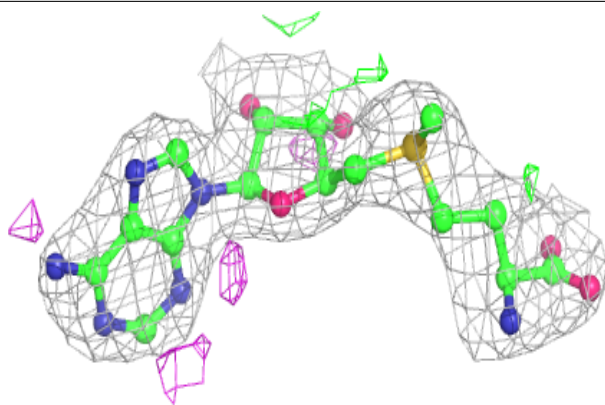
Electron density around SAM B 1001:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around SAM A 1001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.